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(54) Title: A PSEUDO-SEQUENCE METHOD FOR COMPARING 7TM RECEPTORS WITH RESPECT TO THE PHYSICO-CHEMICAL PROPERTIES OF THEIR BINDING SITES

(57) Abstract: A pseudo-sequence method for comparing 7TM receptors with respect to the physicochemical properties of their binding sites, the method comprising the steps of: (i) optionally, aligning part of or all of the amino acid sequence of the first 7TM receptor with part of or all of the amino acid sequence of the one or more further 7TM receptors, (ii) selecting, in a sequential or non-sequential order, at the most 12 amino acid residues per helix and/or extracellular loops, which are involved in one or more binding sites of each 7TM receptor. (iii) forming a pseudo-sequence comprising at the most 50 amino acid residues from the selected sequential or non-sequential amino acid residues, (iv) for each 7TM receptor assigning one or more physicochemical descriptors to the amino acid residues of the selected amino acid pseudo-sequence involved in one or more binding sites, (v) optionally, for each 7TM receptor mathematically manipulating the physicochemical descriptors of step (iv) to obtain a simplified measure of the physicochemical properties of the binding site. (vi) for each 7TM receptor generating a similarity score as defined herein by comparing the physicochemical descriptor or, if relevant, the simplified measure for the one or further 7TM receptors, (vii) optionally, ranking the 7TM receptors with respect to the physicochemical properties of their binding sites according to the similarity scores obtained in step vi)

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